

Compatible Estimators of the Components of Change for a Rotating Panel Forest Inventory Design

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Abstract: This article presents two approaches for estimating the components of forest change utilizing data from a rotating panel sample design. One approach uses a variant of the exponentially weighted moving average estimator and the other approach uses mixed estimation. Three general transition models were each combined with a single compatibility model for the mixed estimation approach. The four resulting estimation systems are compared and contrasted in a sample simulation study covering four simulated populations. *FOR. SCI.* 53(1): 50–61.

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ERIKSSON (1995) gave a set of definitions for the components of forest change that was applicable over a temporal continuum as opposed to the traditional sample-based definitions (e.g., see Meyer 1953) defined over discrete periods.

We use a discrete analog to the Eriksson definitions that facilitates a matrix approach to population definitions. The underlying assumption is that there exists a minimal temporal unit for which an observation of change is either practical or possible. The value of the Eriksson definitions did not so much lie in their absolute temporal continuity as in their independence of the time of observation and the sample design. Eriksson (1995) was seminal in that the traditional definitions of the components of growth were not based strictly on population parameters. For instance, the traditional component of ingrowth can be partitioned into (1) the value of the ingrowth trees as they enter the population, and (2) the value growth subsequent to entering the population. Eriksson (1995) identified the latter partition as a component of survivor growth, using the argument that the tree is a survivor once it has entered the population, regardless of whether or not the entry was observed.

Before considering the sample design, we define (1) Live tree growth as the growth in value that occurs on trees after a defined entry criterion has been achieved; (2) Entry as the value of trees as they attain the entry criterion; (3) Mortality as the value of trees as they die; and (4) Harvest as the value of trees as they are harvested. Eriksson's (1995) definitions were purposefully continuous to ensure additivity, no matter how small a temporal interval one considered. In this article I use a discrete analog to the Eriksson definitions with a small (1-year) interval length. The discrete definitions are motivated by (1) an assumption that 1 year is about the minimum interval length, in most forest conditions, required for each of the respective change signals to overpower measurement error; (2) the need for some reasonable tem-

poral partitioning of the observations; and (3) a desire to facilitate a matrix-based definition of the population.

The Population

The sampled population is three-dimensional; two dimensions are land area and the third is time. Trees exist within this spatial-temporal volume and constitute an associated population of interest. The population of trees (or measures on them) can be partitioned into subpopulations defined by partitions of the original sampled population and/or by attributes of the trees themselves. Below we focus mainly on the temporal dimension of the population and partition the tree population annually, and further subdivide the annual subpopulations by the component of change associated with each tree. Let N = the total number of trees that are in the population during a specific temporal period, and P = the number of years in the population ($t \leq P$).

Define I_E to be an $(N \times P)$ indicator matrix for trees as they enter the population during the forest inventory. In I_E , and all subsequent population matrices, each column represents a year, the first column being the final year of the population of interest, and each successive column 1 year before the previous column. Each row corresponds to an individual tree in the population. That is, a 1 in row i and column j indicates that tree i entered the population in year j . All other entries in row i are zeros. Similarly define the indicator matrices for tree mortality year, I_M , and tree harvest year, I_H , allowing a 1 to indicate the year in which a tree died or was harvested, respectively. The indicator matrix for the live category, I_L , also has one row for each tree and contains a 1 in the column for each year that a tree is alive and in the population of interest subsequent to the entry year and prior to its year of harvest or death, and a zero otherwise. The four indicator matrices are of equal dimension and sum to the population indicator matrix, I_P , as shown in the example in the Appendix.

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The Value of Interest.—Associated with each subdivision of the population of trees is a value of interest. We define the $(N \times P)$ value matrix \mathbf{V} , analogously structured to those above, in that row i represents tree i , and column j represents time j in reverse annual order from the final year P back to year 1. The column vector of \mathbf{V} corresponding to year h is represented as \mathbf{v}_h . Assuming that each tree only enters once, the entry value can be represented by a column vector, \mathbf{v}^E , containing a row for each tree.

Estimands of Interest.—We define two temporal selection matrices. The superior selection matrix, $\widehat{\mathbf{S}}$, has $P - 1$ columns and P rows, such that in column i , row i contains a 1, and all other entries are zero. The final row is all zeros. The inferior selection matrix, $\check{\mathbf{S}}$, has P columns and P rows, such that in the first $P - 1$ columns, i , row $i + 1$ contains a 1 and all other entries are zero. The first row and last column contain all zeros. We also define the first difference matrix, \mathbf{D} , with P columns and P rows, such that in the first $P - 1$ columns, i , row i contains a 1 and row $i + 1$ contains a negative 1, and all other entries are zero. The final column contains all zeros.

We are interested in estimators of the temporal vectors of population change components:

Entry:

$$\mathbf{e}_{P,2} = \widehat{\mathbf{S}}'(\mathbf{I}_E \mathbf{v}^E)$$

Live growth:

$$\mathbf{I}_{P,2} = [(\mathbf{I}_L * (\mathbf{V}\mathbf{D})) + [\mathbf{I}_E * (\mathbf{V} - \mathbf{v}^E)]]\widehat{\mathbf{S}}'\mathbf{1},$$

where $*$ represents element-by-element matrix multiplication, $(\mathbf{V} - \mathbf{v}^E)$ indicates subtraction of the column vector, \mathbf{v}^E , from each column of the matrix \mathbf{V} , and $\mathbf{1}$ is an $(N \times 1)$ summation vector of ones.

Mortality:

$$\mathbf{m}_{P,2} = [(\mathbf{I}_M * (\mathbf{V}\check{\mathbf{S}}))\check{\mathbf{S}}']\mathbf{1}$$

Harvest:

$$\mathbf{h}_{P,2} = [(\mathbf{I}_H * (\mathbf{V}\check{\mathbf{S}}))\check{\mathbf{S}}']\mathbf{1}.$$

We also seek estimators of the total value vector at times P to 1: $\mathbf{v}_{P,1} = (\mathbf{I}_P * \mathbf{V})'\mathbf{1}$. The Appendix contains a worked example of these definitions.

The Rotating Panel Design

Here we focus on estimating the components of change over a defined area and temporal period using a rotating panel annual inventory design, such as the design being used by the USDA Forest Service's Forest Inventory and Analysis (FIA) Units (e.g., see Roesch and Reams 1999). In designs of this type, the sample units are assigned to one of g mutually exclusive temporal panels. One panel is measured per year for g consecutive years, after which the panel measurement sequence reinitiates. That is, if panel 1 is measured in 2007, it will also be measured in 2007 + g , 2007 + 2 g , and so on. Panel 2 would then be measured in 2008, 2008 + g , 2008 + 2 g , etc.

Without loss of generality, we will assume that the

population is uniquely partitioned into K units, indexed $k = 1$ to K , with each unit having a known probability of inclusion in the sample, $\pi_k = a_k/A_K$ (where a_k is the area of unit k , and A_K is the total area of interest). Trees exist on and are uniquely assigned to one and only one unit, and all trees are measured on selected units. For simplicity, assume that a unit's assignment to temporal panel p is random, with probability equal to $1/g$. In this case, the joint probability of selection of unit k in panel z is then $\pi_{kz} = \pi_k/g$. Let the sample panel be represented by an $N \times N$ diagonal matrix, Ψ , indexed as above for each tree in the population, $i = 1, \dots, N$, such that row i , column i contains a 1 if tree i is selected for sample panel p , and a zero otherwise. Represent the panel z sample as $\Psi_z = \Psi \mathbf{I}_p$.

Let the probability of the panel sample be represented by an $N \times N$ diagonal matrix, Π_z , indexed as above for each tree in the population, $i = 1, \dots, N$, such that row i , column i contains π_{kz}^{-1} for tree i in unit k and any panel z , and a 0 otherwise.

With this overlapping panel design, the measurement interval is g years and the minimum growth period that we are recognizing is 1 year. Therefore, between panel measurements, a tree can contribute to multiple components of change. For example, an individual may enter the population, live for 2 years, and then die between observation instances. For a suggestion for estimation to be efficient, the approach must account for a measurement interval length that is longer than the minimum growth interval and it must capitalize on the annually overlapping measurement intervals that result from the rotating panel design.

Estimation

Especially in a rotating panel design, there are potentially many periods of interest within the overall population, so we generalize the above discussion by allowing h to equal the initial year in a specific period of interest, and t to equal the number of annual intervals of interest. We form $\mathbf{y}_{h+t,h}$, a $(P \times 1)$ temporal vector containing a 1 in rows corresponding to years within a specific period of interest (such as $h + t$ to h) and zeros in all other rows, indexed by the endpoints of the period of interest.

In this design, in each panel, we observe the vectors $\psi_E^t = \Psi \mathbf{I}_E \mathbf{y}_{h+t,h+1}$, $\psi_M^t = \Psi \mathbf{I}_M \mathbf{y}_{h+t,h+1}$, and $\psi_H^t = \Psi \mathbf{I}_H \mathbf{y}_{h+t,h+1}$ for entry, mortality, and harvest, respectively. For live growth let $\mathbf{f} = \Psi \mathbf{I}_L \mathbf{y}_{h+t,h+1}$, where \mathbf{f} is a column vector of length N . Form another column vector of length N , ψ_L^t , the observation vector due to the sample. For $i = 1$ to N , let $\psi_L^t[i] = 1$ if $\mathbf{f}[i] = t$.

Within-Panel Estimators.—For within panel estimators we define the period of interest to be the time between the measurements of the panel, so h equals the year of the initial measurement and t is equal to the cycle length or number of years until the next measurement.

Entry

Although we desire estimates for the vector $\mathbf{e}_{h+t,h+1}$, we actually observe an estimate of the scalar sum of the elements of this vector over the years between panel measurements. We label the scalar sum as $E_{h+t,h+1}$. If we assume

that a basic entry value is solely dependent on an entry criterion (such as dbh), the measurement of entry trees during each panel remeasurement provides an estimate of both $E_{h+t,h+1}$ and the growth on the entry trees ($E_{h+t,h+1}^g$) subsequent to entry. The strictly sample-based per-panel estimator for $E_{h+t,h+1}$ would be $\hat{E}_{h+t,h+1} = (\Pi_z \psi_E^t)' \mathbf{v}_E$.

$\hat{E}_{h+t,h+1}$ is a biased estimator of $E_{h+t,h+1}$ because it does not include trees that became eligible and subsequently died or were harvested between observations. The sample estimate at time $h + t$ of trees entering the population between times h and $h + t$ would be

$$\tilde{E}_{h+t,h+1} = (\Pi_z \psi_E^t)' \mathbf{v}_{h+t}.$$

The per-panel estimator for growth on entry ($E_{h+t,h+1}^g$) can be expressed as

$$\hat{E}_{h+t,h+1}^g = \tilde{E}_{h+t,h+1} - \hat{E}_{h+t,h+1}.$$

Mortality

As with entry, we desire estimates for the mortality vector $\mathbf{m}_{h+t,h+1}$; however, we actually observe a scalar sum over the years between panel measurements. Consider the sum of the elements of $\mathbf{m}_{h+t,h+1}$, label it $M_{h+t,h+1}$, and assume that mortality trees cannot be reliably measured. We might estimate $M_{h+t,h+1}$ with the biased estimator

$$\tilde{M}_{h+t,h+1} = (\Pi_z \psi_M^t)' \mathbf{v}_h.$$

Value is unobserved for mortality trees past year h and, therefore, the value at the year of death ($h + d$) for tree i ($v_{d,i}$) would have to be modeled. For a model-based estimator, form the column vector \mathbf{v}_d^g , in which element i for tree i is equal to $v_{h+t,h+1} - v_{h,i}$, if the row i in ψ_M^t contains a 1. Assuming an estimator of \mathbf{v}_d^g , $\hat{\mathbf{v}}_d^g$, $\tilde{M}_{h+t,h+1}$ could be formed by $\hat{M}_{h+t,h+1} = \tilde{M}_{h+t,h+1} + \hat{M}_{h+t,h+1}^g$, where $\hat{M}_{h+t,h+1}^g = \psi_M^t' \hat{\mathbf{v}}_d^g$. Even if $\hat{M}_{h+t,h+1}^g$ is unbiased, like $\hat{E}_{h+t,h+1}$, $\hat{M}_{h+t,h+1}$ is a biased estimator, owing to the unobserved subpopulation of trees that becomes eligible and subsequently dies between observations.

Harvest

As with the previous two components, sum the elements of $\mathbf{h}_{h+t,h+1}$ to produce $H_{h+t,h+1}$ and assume that mortality trees cannot be reliably measured. A biased per-panel estimator for $H_{h+t,h+1}$ could be expressed as $\tilde{H}_{h+t,h+1} = (\Pi_z \psi_H^t)' \mathbf{v}_h$. As with mortality, the value at the year of harvest ($h + c$), for tree i ($v_{h+c,i}$) is unobserved and would have to be modeled conditional on the value at year h ($v_{h,i}$). Form the column vector \mathbf{v}_H^g , in which element i for tree i is equal to $v_{h+c,i} - v_{h,i}$ if the corresponding row in ψ_H^t contains a 1. Given an unbiased estimator of \mathbf{v}_H^g , $\hat{\mathbf{v}}_H^g$, $\hat{H}_{h+t,h+1}$ would be obtained by $\hat{H}_{h+t,h+1} = \tilde{H}_{h+t,h+1} + \hat{H}_{h+t,h+1}^g$, where $\hat{H}_{h+t,h+1}^g = (\Pi_z \psi_H^t)' \hat{\mathbf{v}}_H^g$. As with the previous two estimators, if $\hat{H}_{h+t,h+1}^g$ is unbiased, then $\hat{H}_{h+t,h+1}$ is a biased estimator, because it cannot include trees that became eligible, and were subsequently harvested, between observation instances.

Live Growth

Define the true value matrix for panel remeasurement z (\mathbf{V}_z) from the values of the population of trees at times $h +$

t and h , by selecting the two corresponding columns from \mathbf{V} . That is, row i represents tree i , and column j represents time $j = h + t$ and h :

$$\mathbf{V}_z = \begin{bmatrix} v_{1,h+t} & v_{1,h} \\ v_{2,h+t} & v_{2,h} \\ \vdots & \vdots \\ \vdots & \vdots \\ v_{N,h+t} & v_{N,h} \end{bmatrix}$$

Additionally, we define the panel difference vector with 1 column and 2 rows: $\mathbf{d} = \begin{bmatrix} 1 \\ -1 \end{bmatrix}$.

An estimator for live growth per panel would be

$$\begin{aligned} \hat{L}_{h+t,h+1} &= (\mathbf{V}_z \mathbf{d})' (\Pi_z \psi_L^t) + \hat{E}_{h+t,h+1}^g \\ &\quad + \hat{M}_{h+t,h+1}^g + \hat{H}_{h+t,h+1}^g. \end{aligned}$$

Again, as with the previous estimators, $\hat{L}_{h+t,h+1}$ will be biased by the value of growth on trees that became eligible and then died or were harvested between observation instances.

The bias in each of these components will often be small for two reasons: (1) the contribution to the bias comes from relatively small trees, and (2) trees within 5 years of having reached eligibility that die or are harvested are a relatively small component of many forest populations. The smaller the investigator's area of interest and the stronger the market forces to harvest trees in that area of interest, the greater will be the risk in ignoring the bias in these components.

Combining Panels.—The overlapping panels in the rotating panel design facilitate many options for estimating the component change vectors by combining the within-panel estimates. Additionally, the observation that sample sizes within panels are often too small to provide low variance estimates within many geographic subareas of interest leads to the question of how we might draw strength from adjacent time intervals by combining panels. We will discuss two approaches, an exponentially weighted difference (EWD) estimator and a mixed estimator.

Exponentially Weighted Difference

One possible strategy I'll dub an exponentially weighted difference (EWD) estimator, owing to its similarity in concept to the exponentially weighted moving average (EWMA) estimator common in the quality control literature (i.e., Chandra 2000) and the econometrics literature (i.e., West and Harrison 1989, p. 55). In this proposed EWD estimator, a series of differences (i.e., a series of change component panel sums) within panels is calculated. The EWD gives larger weights to the interval observations closest to being centered on the interval of interest, allowing more local variation than if equal weights are used. In the EWD estimator (d_k') below, the panel difference is centered on the interval and combined with the $m - 1$ adjoining interval differences. The supporting panels are down-weighted exponentially with each step away from the central panel.

Let

$\bar{d}_{h+t,h+1}$ = the mean of a remeasured panel difference,
such as $t^{-1}\hat{L}_{h+t,h+1}$

$r = (m - 1)/2$, m is odd and is the number of
remeasured panels used
in the estimator, and

$$\alpha = \left(\frac{r}{r+1} \right).$$

The EWD estimator, applied to year k , is

$$d'_k = \sum_{i=-r}^r \frac{1-\alpha}{1+\alpha-2\alpha^{r+1}} \alpha^{|i|} \bar{d}_{k+r+i,k-r+i}.$$

One can see that the EWD estimator discounts distant panels exponentially because increasing values of $|i|$ result in the weight being smaller, since $r/(r+1)$ is less than 1. One method of assuring compatibility when using this estimator would be to estimate entry, live growth, mortality, and harvest separately, and then use the sum of these component vectors to estimate the total value vector. Although the resulting system would be compatible, the individual estimators would not be optimized in any way. Additionally, the EWD provides no estimates for m years on each end of the time string. In practice, an ad hoc variation would have to be incorporated to provide some or all of these estimates.

Mixed Estimation

The mixed estimator (e.g., Van Deusen 1996, Theil 1963) can also be used to draw strength from overlapping panels. Korhonen (1993) used mixed estimation for calibrating tree volume functions. Van Deusen (1996, 1999, 2000) showed mixed estimators for annual forest inventory designs. In this work, we use mixed estimation to simultaneously estimate the trends for the four components of change and constrain the sum of the changes to equal the estimate for total change. The components of change estimators are compatible if, for any initial year i and any time interval t ,

$$\hat{V}_{i+t} - \hat{V}_i = \hat{L}_{i+t,i+1} + \hat{E}_{i+t,i+1} - \hat{M}_{i+t,i+1} - \hat{H}_{i+t,i+1}.$$

A rotating panel design (with k panels) is conducive to a model in which the observed midpoint values for the total change are used to constrain the component estimates. For k , an integer, and $t \geq k+1$, let

$$\delta_i^k = \begin{cases} (V_{t-(k-1)/2} - V_{t-(k+1)/2}), & \text{if } k \text{ is odd;} \\ (V_{t-(k-2)/2} - V_{t-(k+2)/2}), & \text{if } k \text{ is even;} \end{cases}$$

and form a five-row column vector χ_t^k such that:

$$\chi_t^k = \begin{cases} \delta_i^k \begin{vmatrix} L_{t,t-k+1} & E_{t,t-k+1} & M_{t,t-k+1} & H_{t,t-k+1} \\ k & k & k & k \end{vmatrix} & \text{if } k \text{ is odd} \\ \delta_i^k \begin{vmatrix} 2L_{t,t-k+1} & 2E_{t,t-k+1} & 2M_{t,t-k+1} & 2H_{t,t-k+1} \\ k & k & k & k \end{vmatrix} & \text{if } k \text{ is even.} \end{cases}$$

Assume an observation model for time t .

$$\chi_t^k = \beta_t + e_t, \quad (1)$$

where β_t is a column vector of five coefficients, β_t^i (where $i = 1, \dots, 5$), with a column for each component in χ_t^k and e_t is a five-row column vector of e_t^i that are iid $(0, \sigma_{e,t}^2/m_t)$, and combine it with a set of constrained compatibility and transition models, such as

$$\beta_t^1 - \beta_t^2 - \beta_t^3 + \beta_t^4 + \beta_t^5 = \varepsilon_{1,t}, \quad t \geq k+1; \quad (2a)$$

$$\beta_t^2 - 2\beta_{t-1}^2 + \beta_{t-2}^2 = \varepsilon_{2,t}, \quad t \geq k+3; \quad (2b)$$

$$\beta_t^3 - 2\beta_{t-1}^3 + \beta_{t-2}^3 = \varepsilon_{3,t}, \quad t \geq k+3; \quad (2c)$$

$$\beta_t^4 - 2\beta_{t-1}^4 + \beta_{t-2}^4 = \varepsilon_{4,t}, \quad t \geq k+3; \quad (2d)$$

$$\beta_t^5 - 2\beta_{t-1}^5 + \beta_{t-2}^5 = \varepsilon_{5,t}, \quad t \geq k+3; \quad (2e)$$

where $\varepsilon_{i,t}$ is iid $(0, \sigma_{\varepsilon,t}^2/m_t)$. Compatibility between the components and total change is constrained with (2a), and the transition from year to year for each component, in turn, is constrained with Equations 2b through 2e.

Form a vector χ from the χ_t^k values having $((T-k)*5)$ rows. Concatenate successive elements of the column vectors β_t into the column vector

$$\beta = \begin{bmatrix} \beta_{k+1} \\ \vdots \\ \beta_T \end{bmatrix}, \quad \text{having } ((T-k)*5) \text{ rows.}$$

Form vectors by stacking the successive vectors of error terms:

$$e = [e_{k+1}, \dots, e_T]' \quad \text{and} \quad \varepsilon = [\varepsilon_{k+1}, \dots, \varepsilon_T]'$$

Represent Equation 1 with

$$\chi = \beta + e$$

Represent the covariance matrix of χ with Σ . The constraints can be re-expressed

$$R\beta = \varepsilon$$

where R is the matrix of constraints for the compatibility and transition models.

Combining the models results in the solution set for a mixed estimator,

$$\begin{bmatrix} \chi \\ 0 \end{bmatrix} = \begin{bmatrix} I \\ R \end{bmatrix} \beta + \begin{bmatrix} e \\ \varepsilon \end{bmatrix}.$$

In this formulation, we can use the same assumptions as Van Deusen (1999). Applying the constraints strictly, the mixed estimator is $\hat{\beta} = \chi - \Sigma R' [R \Sigma R']^{-1} R \chi$.

Simulation

The Population Simulations.—FIA data from field inventory plots measured in 1968 and remeasured in 1981 in Hancock County, Maine, were used as seed data for four artificial populations of species group, dbh, life stage, and location attributes. The four populations are intended to represent a realistic diversity in relationships between the

components rather than to represent any specific real populations. The species groups are defined in Table 1. The temporal dimension of each of the populations was 25 years. The remeasurement data were used to establish initial tree basal area (ba) growth, mortality, harvest, and entry rates. The four populations differed in their deviance from these initial observations as described below.

Initially, the individual plot data of all trees of at least 5 inches in dbh from 1981 were coalesced into a square population (Pop1), as described in Roesch (1993). In this simulation, a population area of 100 times the area of Pop1 was created by using Pop1 to seed each element of a 10×10 matrix (Pop2). During each seed event for Pop2, a random variate was added to each tree's basal area and location in Pop1. The basal area variate was drawn from a uniform distribution, $U(0.9 \text{ ba}, 1.1 \text{ ba})$. Each tree's x and y coordinates were also displaced by a uniform random variable with a range of ± 0.914403 meters. The final location of a tree would therefore sometimes be in an adjacent matrix "pixel" and sometimes it would be located outside of the population area. In the latter case, the point was wrapped around to the other side of the population area, as if the population's edges were joined. This was done four times to establish year 1 for each of the four populations. Species-group specific annual growth rates, calculated from the original permanent plot data (see Table 2), were applied to each tree annually after adjustment of the slope parameter by a normal zero-mean random variate. That is, for tree i in species group s at time $t + 1$, draw a variate v_i from an $N(0, 1)$ distribution and then calculate an adjusted slope parameter $a_{2,i} = a_{1,s} + 0.1v_i(a_{1,s} - 1.0)$. Then calculate the basal area of tree i for time $t + 1$, $ba_{i,t+1} = a_{0,s} + a_{2,i}ba_{i,t}$. Each year, in each population, harvest and mortality were randomly applied at differing target rates in proportion to live basal area [The tables of target proportions of basal area harvested and mortality per year for each population are available for the interested reader from the author]. The target harvest rates were generally high in populations 1 and 2 and low in populations 3 and 4, except for an anomaly in year 13 in population 4. The anomaly represents a large salvage cut that necessitated the removal of live trees the year following a large mortality event. The target harvest rates were steadily increased in population 1, and first increased and then decreased in populations 2 and 3. In population 4, the target harvest rates were steadily increased until the anomaly, reduced after the anomaly, and then steadily increased. The mortality rates were generally high

Table 2. Initial parameter coefficients and number of sample trees (n) used to establish the 1-yr ahead basal area (m^2) projections for the model $BA_{t+1} = b_0 + b_1BA_t$

Species group (s)	$a_{0,s}$	$a_{1,s}$	n
1	4.9875×10^{-4}	1.01983321	23
2	2.4545×10^{-4}	1.01788948	300
3	1.0377×10^{-4}	1.01938054	63
4	2.2649×10^{-4}	1.02565698	44
5	1.1369×10^{-4}	1.01518667	181
6	2.4461×10^{-4}	1.01334942	212
7	4.7587×10^{-4}	1.00857833	35
8	9.4644×10^{-5}	1.01836823	64
9	3.2909×10^{-4}	1.01225738	75

in populations 1 and 2 and low in populations 3 and 4, except for anomalies in year 12 for populations 3 and 4. The 40% mortality events in these populations for year 12 might result in areas subjected to an extremely large and destructive hurricane. The mortality rates were steadily decreased in population 1, and first increased and then decreased in population 2. In populations 3 and 4, the mortality rates were steadily increased until the anomaly, reduced after the anomaly, and then steadily increased again. Entry was assumed to lag behind harvest and mortality at the rate of 1.6 entry trees per harvested tree and 0.5 entry tree per mortality tree.

The resulting population trends are given in Figures 1 and 2. Figure 1 graphs the total basal area for each population over the 25-year span. Figure 2 graphs the live growth, harvest, mortality, and entry for years 2 through 25 in a separate graph for each population. The large anomalies in populations 3 and 4 are listed separately for clarity.

The Sample Simulations.—Thirty random points were selected from the population area for each of five sample panels. This was done 200 times. Each point selected all population trees within a radius of 7.315 meters. Exact panel inclusion probabilities were used in all estimators for each sample tree. Obviously, for most trees, this was equal to the area of a 7.315 m radius circle divided by the area of the population. For trees closer to the edge of the population than 7.315 m, the numerator was reduced by the tree area falling outside of the population area, because a tree could only be selected from within the population area. The panels were applied in sequence annually, and then re-observed in the same sequence continuously. The simulation compared the exponentially weighted difference estimator and the

Table 1. Species members of the nine species groups

Species Group	Species		
1	<i>Pinus banksiana</i>	<i>Pinus resinosa</i>	<i>Pinus strobus</i>
2	<i>Picea glauca</i>	<i>Picea mariana</i>	<i>Picea rubens</i>
3	<i>Abies balsamea</i>		
4	<i>Larix laricina</i>	<i>Tsuga canadensis</i>	
5	<i>Thuja occidentalis</i>		
6	<i>Acer pennsylvanicum</i>	<i>Acer rubrum</i>	<i>Acer saccharum</i>
7	<i>Fraxinus americana</i>	<i>Fraxinus nigra</i>	<i>Ostrya virginiana</i>
	<i>Populus grandidentata</i>	<i>Populus tremuloides</i>	<i>Tilia americana</i>
8	<i>Fagus grandifolia</i>	<i>Prunus serotina</i>	<i>Quercus rubra</i>
9	<i>Betula alleghaniensis</i>	<i>Betula papyrifera</i>	<i>Betula populifolia</i>

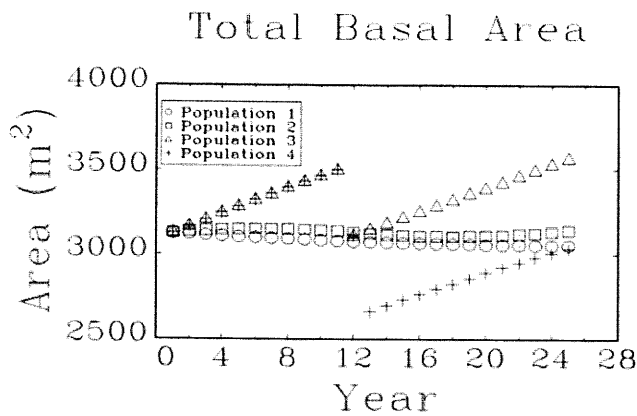


Figure 1. The total basal area (m^2) for years 1 through 25 for the four simulated populations.

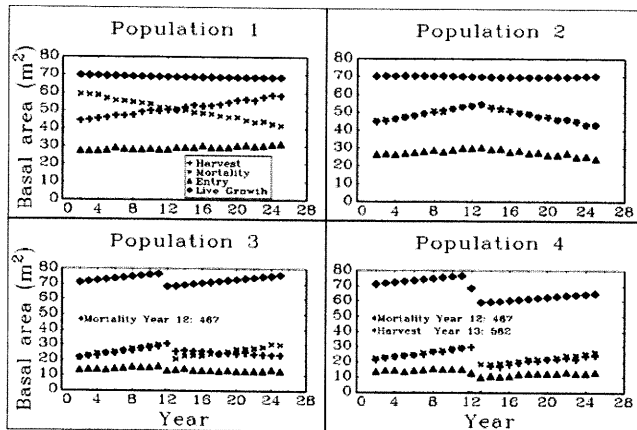


Figure 2. The basal area of live growth, entry, mortality, and harvest (m^2) for years 2 through 25 for the four simulated populations.

mixed estimator for estimating the components of basal area change and total basal area change. There was no effort to enforce compatibility constraints for the EWD estimates. Three general candidate models were considered for the mixed estimator.

For all three of the candidate models an initial estimate of total basal area was obtained using the sample mean for each of the 25 years. The series of 21 5-year equally weighted moving averages (EMA) was calculated from these initial estimates. The first differences of the EMA estimates were taken in succession, resulting in 20 estimates of change in total basal area $BA(t) - BA(t - 1)$, where $t = 4, \dots, 23$.

The 25-year series provides 20 initial estimates for each component, commencing with the year of the first panel remeasurement in year 6. From this, 16 consecutive 5-year equally weighted moving averages were calculated for each component. These were assumed to correspond to vector positions 3 to 18 of the basal area difference vector. The remaining positions were filled with the most supported centralized estimate available. In the cases of positions 1 and 20, this was the corresponding initial estimate for the component. For positions 2 and 19, a 3-year average was used, e.g., initial estimates 1 through 3 for position 2, and initial estimates 18 through 20 for position 19. This resulted in 20 estimates of total basal area change and 20 estimates

of the corresponding change components, live growth, entry, mortality, and harvest.

Constraints.—The compatibility constraints in Equation 2a, constraint set A, were applied to all three candidate models. The models differed in the component transition constraints, constraint set B, appended to the compatibility constraints. Next, we give the three general models and note exceptions below the general models.

In model 1, the transition constraints are identical to Equations 2b through 2e above, with $t \geq k + 3$:

$$\beta_t^2 - 2\beta_{t-1}^2 + \beta_{t-2}^2 = \varepsilon_{2,t};$$

$$\beta_t^3 - 2\beta_{t-1}^3 + \beta_{t-2}^3 = \varepsilon_{3,t};$$

$$\beta_t^4 - 2\beta_{t-1}^4 + \beta_{t-2}^4 = \varepsilon_{4,t};$$

$$\beta_t^5 - 2\beta_{t-1}^5 + \beta_{t-2}^5 = \varepsilon_{5,t}.$$

In model 2, with $t \geq k + 4$, the transition constraints are

$$\beta_t^2 - 3\beta_{t-1}^2 + 3\beta_{t-2}^2 - \beta_{t-3}^2 = \varepsilon_{2,t};$$

$$\beta_t^3 - 3\beta_{t-1}^3 + 3\beta_{t-2}^3 - \beta_{t-3}^3 = \varepsilon_{3,t};$$

$$\beta_t^4 - 3\beta_{t-1}^4 + 3\beta_{t-2}^4 - \beta_{t-3}^4 = \varepsilon_{4,t};$$

$$\beta_t^5 - 3\beta_{t-1}^5 + 3\beta_{t-2}^5 - \beta_{t-3}^5 = \varepsilon_{5,t}.$$

In model 3, with $t \geq k + 5$, the transition constraints are

$$\beta_t^2 - 3\beta_{t-1}^2 + 4\beta_{t-2}^2 - 3\beta_{t-3}^2 + \beta_{t-4}^2 = \varepsilon_{2,t};$$

$$\beta_t^3 - 3\beta_{t-1}^3 + 4\beta_{t-2}^3 - 3\beta_{t-3}^3 + \beta_{t-4}^3 = \varepsilon_{3,t};$$

$$\beta_t^4 - 3\beta_{t-1}^4 + 4\beta_{t-2}^4 - 3\beta_{t-3}^4 + \beta_{t-4}^4 = \varepsilon_{4,t};$$

$$\beta_t^5 - 3\beta_{t-1}^5 + 4\beta_{t-2}^5 - 3\beta_{t-3}^5 + \beta_{t-4}^5 = \varepsilon_{5,t}.$$

Adjustments for Populations 2, 3, and 4

It was assumed that there was some prior but incomplete knowledge of the anomalies that occurred in populations 2, 3, and 4. In these populations, the rows in constraint set B corresponding to the constraints for the affected change components that crossed the year(s) of the anomaly were deleted. The anomalies adjusted for were the general trend reversal for harvest and mortality subsequent to year 13 in population 2, the large mortality events in year 12 in populations 3 and 4, and the large harvest event in year 13 in population 4. In population 2, it was assumed that all components were affected by the general change in trend for harvest and mortality in models 1 and 2, so all constraints in set B that crossed year 13 were deleted. In model 3, only the constraints for harvest and mortality crossing year 13 were deleted. For population 3, it was assumed that all components were affected by the large mortality event in year 12 in models 1 and 2, so all constraints in set B that crossed year 12 were deleted. In model 3, only the constraints for mortality, live growth, and entry crossing year 12 were deleted. That is, the harvest constraints were not deleted. In population 4, it was assumed that all components were affected by the large mortality event in year 12 and the

large harvest event in year 13 in all three models, so all constraints in set B that crossed years 12 and 13 were deleted.

Additionally, the large mortality event in year 12 for populations 3 and 4, and the subsequent harvest event of live trees in population 4, suggest that those years should not be included as endpoints for the assumed affected components either. Therefore, those rows were also deleted. Data from across the anomaly years were not combined in the initial estimates for the affected components or total change in basal area. That is, a single panel's estimate was used in the anomaly year and surrounding years treated as endpoints. A 3-year average or a single-year's mean replaced the 5-year moving average in the initial estimates, where appropriate.

The four estimators (the EWD estimator and the three candidate models for the mixed estimator) for each component were calculated for each of the 200 sample simulations drawn from each population. The mean-squared difference (MSD) and mean difference (MD) between each of the four estimators and the true values for each of the 20 intervals of interest beginning with years 3–4 and culminating with years 22–23 were calculated.

Simulation Results

For total basal area change and the four components of change, Figures 3 through 7 give the mean-squared differences (MSD) and mean differences (MD) between the four estimators (the EWD estimator and the three candidate models for the mixed estimator) and the true values for the four populations. For clarity, the results for the candidate models are shown rather than using an information criterion and selecting the "best" model for each sample in the simulation (e.g., as in Van Deusen 1999). Otherwise, simulation estimates from the 200 samples would come from a mixture of model choices, rendering results that would not provide as much insight as the results from the individual models.

Figure 3 shows the statistics for total basal area change; note that all three models used in the mixed estimator have lower values for MSD almost everywhere. The notable exceptions occur near the endpoints. That is, the first and last intervals estimated, and near the anomaly years for populations 2, 3, and 4. In populations 3 and 4, the mixed estimator results are all much better than the EWD results for the years adjacent to the anomaly year(s), but not in the anomaly years. Recall that the EWD is using five panels' worth of data and placing the most weight on the central panel in the anomaly year, while the adjustments to the ME models have resulted in one panel's worth of data being used in the anomaly years. It is suspected that this result concerning the anomalous years is not conclusive; that is, we cannot normally expect better results from combining information across anomalous years, but would rather have an increased sample at times of higher uncertainty. This suspicion is supported by the results for years adjacent to the anomalous years, in that the EWD estimator's MSD

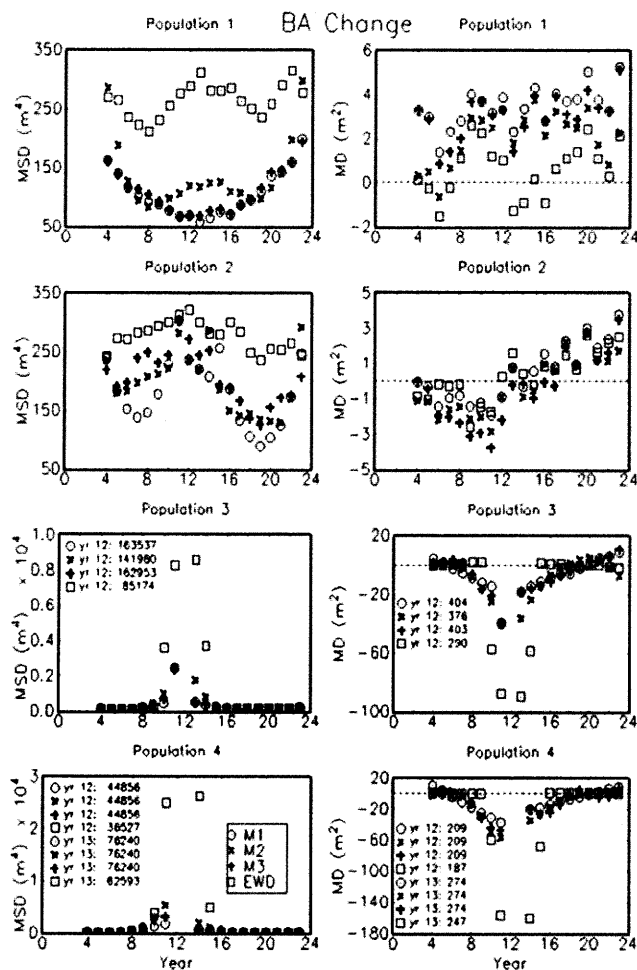


Figure 3. The mean-squared difference (left) and mean difference (right) calculated from 200 five-panel samples (of 30 units per panel) for estimates of basal area change using the exponentially weighted difference estimator and models 1, 2, and 3 for the mixed estimator for years 4 through 23 for the simulated populations.

results are much higher than those for the ME models. In general, the MD results show that there is some distinction between the estimation approaches in the contribution of bias to the MSD. Although the empirical bias in almost all cases is low, we note that the empirical bias (MD) is lower for the EWD estimator during most years in population 1. Extremely low bias in the EWD estimator persists for longer than the ME as the estimates approach the anomaly years in populations 3 and 4. This advantage disappears for 2 years on either side of the anomaly years.

The MSD and MD results for the entry component are given in Figure 4. Many of the same observations can be made by examination of Figure 4 as were made by examination of Figure 3 with respect to the reduction in differences in MSD between the estimators near the temporal endpoints. It also seems clear that the proportional difference in this statistic between the EWD and ME is greater for longer run lengths. That is, the difference is much less distinct in populations 2, 3, and 4, where the run lengths are interrupted by anomalies. Where there is a separation in the MSD results for the ME models for entry, model 2 usually has the highest

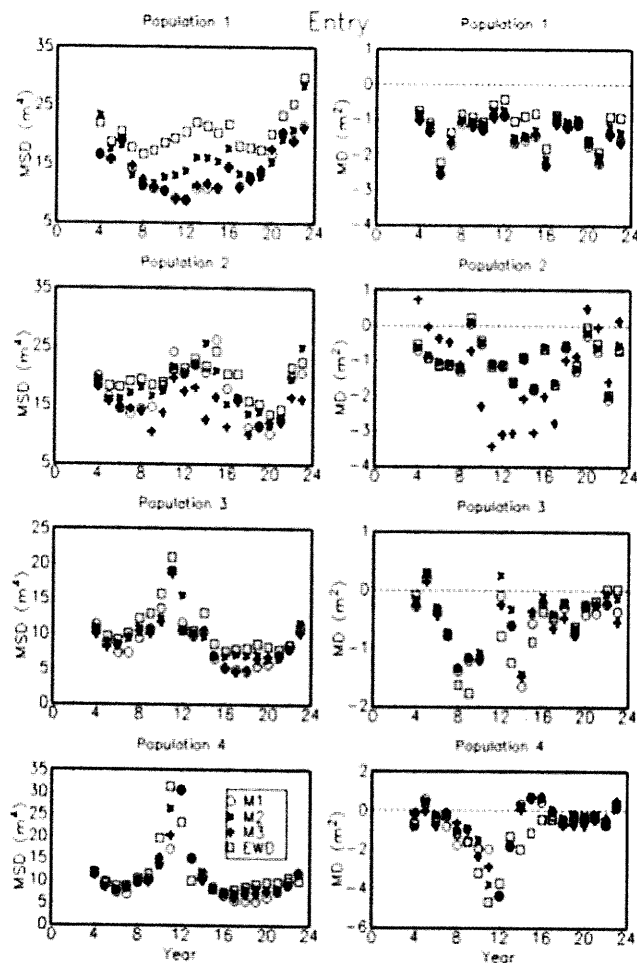


Figure 4. The mean-squared difference (left) and mean difference (right) calculated from 200 five-panel samples (of 30 units per panel) for estimates of entry using the exponentially weighted difference estimator and models 1, 2, and 3 for the mixed estimator for years 4 through 23 for the simulated populations.

value of the three. In population 2, model 3 has the lowest values for MSD across the anomaly years, where there was a change in direction of harvest and mortality trend that would also affect subsequent entry. We also note that bias (MD) increases significantly when the modeling effort approaches the anomaly in population 4.

Figure 5 gives the MSD and MD results for the live growth component. Both in natural populations and in these simulated populations, much of the sample contributes to the live growth component. Examination of the figure shows very good results for both the EWD and the ME by both statistics for populations 1 and 2. This same figure shows the EWD estimator giving better results for MSD and MD, beginning with the anomalous years and lasting until year 18 in population 3 and year 19 in population 4.

The MSD results for the mortality component are shown in Figure 6. Many of the same observations can be made from Figure 6 as were made from the previous figures with respect to the reduction in differences in MSD between the estimators near the temporal endpoints. It again seems clear that the proportional difference in this statistic between the EWD and ME is

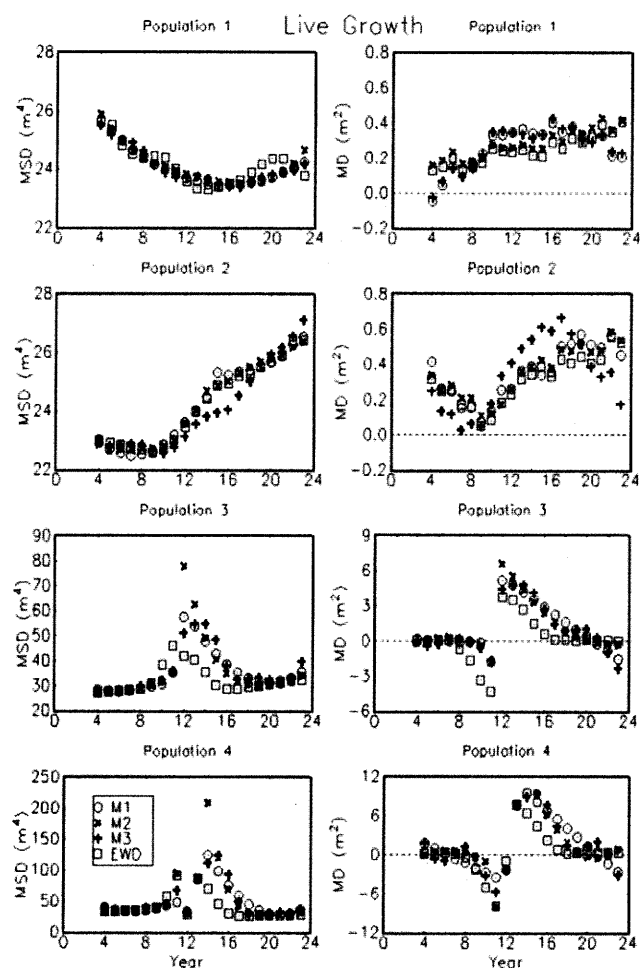


Figure 5. The mean-squared difference (left) and mean difference (right) calculated from 200 five-panel samples (of 30 units per panel) for estimates of live growth using the exponentially weighted difference estimator and models 1, 2, and 3 for the mixed estimator for years 4 through 23 for the simulated populations.

greater for longer run lengths. The difference is much less distinct in populations 2, 3, and 4, where the run lengths are interrupted by anomalies. Where there is a separation in the MSD results for the ME models for mortality, model 2 usually has the highest value of the three. In population 2, model 1 has the lowest values for MSD toward the center of the run lengths prior and subsequent to the change in direction of the mortality trend. This tendency of model 1 to be lowest in MSD toward the center of the run length is present but less pronounced in population 1.

Observe that bias (MD) is usually an insignificant error component with respect to its contribution to total squared error for the EWD estimator. Again, we see a greater prediction bias for the ME models in population 1. This, in conjunction with the lower MSD values for ME in the same ranges, shows a much lower variance for the ME than the EWD estimator, at the cost of a slight increase in bias. Bias becomes the overriding error component for all of the estimators in populations 3 and 4 in the vicinity of the large mortality event of year 12.

Figure 7 gives the MSD and MD results for the harvest component. The majority of observations discussed above

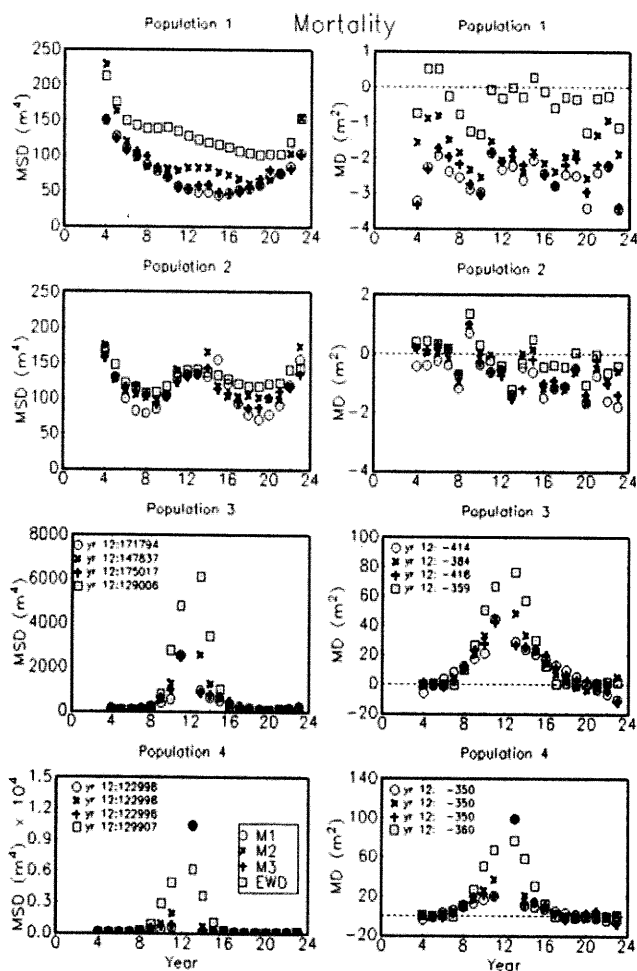


Figure 6. The mean-squared difference (left) and mean difference (right) calculated from 200 five-panel samples (of 30 units per panel) for estimates of mortality using the exponentially weighted difference estimator and models 1, 2, and 3 for the mixed estimator for years 4 through 23 for the simulated populations.

for the other components can be applied directly to the results for harvest. Of special interest are the MSD results for population 3. Recall that in models 1 and 2 for the mixed estimator it was assumed that the large mortality event in year 12 would also affect all of the other components. In model 3, that assumption was not made for harvest, and its constraint rows crossing year 12 were not deleted. Additionally, the full 5-year moving average was used as the initial estimate for harvest each year in model 3, rather than treating year 12 as an endpoint. The much lower MSD for model 3 of the ME, as opposed to models 1 and 2, shows that the effect of the mortality event on harvest was not large enough to justify using fewer panels in the initial harvest estimates surrounding and including year 12.

Conclusion

Although none of the results is alarming in light of the underlying sample used to form the estimates, some of the results that favor the EWD estimator over the ME appear to have more to do with the choice between modeling the components in separate “chains” or using a more flexible model over the entire period, rather than with the choice of

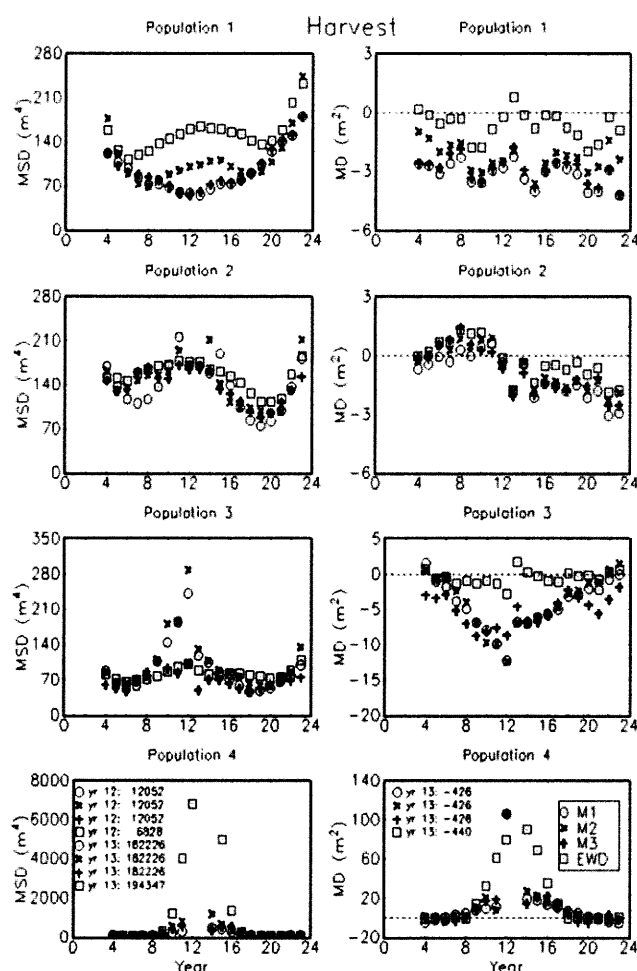


Figure 7. The mean-squared difference (left) and mean difference (right) calculated from 200 five-panel samples (of 30 units per panel) for estimates of harvest using the exponentially weighted difference estimator and models 1, 2, and 3 for the mixed estimator for years 4 through 23 for the simulated populations.

estimation approach. This simply illustrates the basic tenet that there can be a fairly high cost to using a smaller sample, so one should have good reason to choose to define separate subpopulations for estimation. Once that choice has been made, the adequacy of each subpopulation’s sample must be addressed. In the case of populations 3 and 4, the best solution for improving estimates in (and close to) the anomaly years would be to augment the sample with additional data.

There are no strictly design-unbiased estimators for the annual components of change available for temporally rotating panel designs with an observation period longer than 1 year. The mixed estimation technique allows us to use simple models to make well-supported estimates at varying scales for designs of this type by drawing strength from measurements made on temporal “neighbors.” The EWD estimators used here also draw strength from temporal neighbors for the individual components. The significant advantage of the ME technique is that it allows the formal consideration of theoretical relationships between the components in the form of constraints. We did not explore the additional advantage to the ME in that it provides an obvious framework for

the use of an information criterion to choose between different candidate models, as shown by Van Deusen (1999). In practice, an operational inventory should include that capability.

It is often assumed, in practice, that a compatibility requirement will bear some cost in suboptimization of one or more of the component estimates. This study did not attempt to quantify that cost. We note that all of the ME models contained the compatibility constraints (constraint set A), while the EWD estimates were not constrained. The ME models usually performed better in terms of the mean-squared difference statistic but had slightly elevated values for the mean difference statistic. Any cost of compatibility might be assumed to be a component of the latter. Since mean-squared error equals the variance plus bias squared, and the squared error statistic was quite favorable for models enforcing compatibility, we can assume that the cost of compatibility has not been shown to be a significant consideration in this study.

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Appendix

The following is an example of the population component matrices and the estimands that arise from them. Assume that we have of interest a population consisting of five trees over a period of 5 years. Tree 1 is alive and in the population for the entire period. Tree 2 enters during year 3 and survives for the rest of the period. Tree 3 enters during year 1, survives through year 4, and dies during year 5. Tree 4 is alive at the beginning

of the period and harvested during year 4. Tree 5 enters during year 5. We write the population matrix as

$$\begin{array}{rcl} \text{year} & = & \begin{array}{ccccc} 5 & 4 & 3 & 2 & 1 \end{array} \text{Tree} \\ & & \begin{bmatrix} 1 & 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 0 & 0 \\ 1 & 1 & 1 & 1 & 1 \\ 0 & 1 & 1 & 1 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{array}{l} 1 \\ 2 \\ 3 \\ 4 \\ 5 \end{array} \end{array}$$

In turn, we then define each component. The entry matrix is

$$\begin{array}{rcl} \text{year} & = & \begin{array}{ccccc} 5 & 4 & 3 & 2 & 1 \end{array} \text{Tree} \\ & & \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{array}{l} 1 \\ 2 \\ 3 \\ 4 \\ 5 \end{array} \end{array}$$

The live matrix is

$$\begin{array}{rcl} \text{year} & = & \begin{array}{ccccc} 5 & 4 & 3 & 2 & 1 \end{array} \text{Tree} \\ & & \begin{bmatrix} 1 & 1 & 1 & 1 & 1 \\ 1 & 1 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 0 & 1 & 1 & 1 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{array}{l} 1 \\ 2 \\ 3 \\ 4 \\ 5 \end{array} \end{array}$$

The mortality matrix is

$$\begin{array}{rcl} \text{year} & = & \begin{array}{ccccc} 5 & 4 & 3 & 2 & 1 \end{array} \text{Tree} \\ & & \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{array}{l} 1 \\ 2 \\ 3 \\ 4 \\ 5 \end{array} \end{array}$$

Finally, the harvest matrix is

$$\begin{array}{rcl} \text{year} & = & \begin{array}{ccccc} 5 & 4 & 3 & 2 & 1 \end{array} \text{Tree} \\ & & \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{array}{l} 1 \\ 2 \\ 3 \\ 4 \\ 5 \end{array} \end{array}$$

To show that the components completely and uniquely partition the population, we show the population as the simple addition of the four component matrices:

$$\mathbf{I}_P = \mathbf{I}_E + \mathbf{I}_L + \mathbf{I}_M + \mathbf{I}_H$$

$$= \begin{bmatrix} 1 & 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 0 & 0 \\ 1 & 1 & 1 & 1 & 1 \\ 0 & 1 & 1 & 1 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} + \begin{bmatrix} 1 & 1 & 1 & 1 & 1 \\ 1 & 1 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 0 & 1 & 1 & 1 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} + \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} + \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}.$$

We define a value matrix of arbitrary units:

$$\mathbf{V} = \begin{bmatrix} 9 & 8 & 7 & 5 & 3 \\ 3 & 2 & 1 & 0 & 0 \\ 0 & 6 & 4 & 3 & 1 \\ 0 & 0 & 7 & 6 & 5 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix}.$$

In this population, trees always enter with a value of 1, therefore:

$$\mathbf{v}^E = \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix}.$$

The resulting population estimands are:

$$\text{Entry: } \mathbf{e}_{P,2} = \widehat{\mathbf{S}}'(\mathbf{I}_E' \mathbf{v}^E) = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{bmatrix}' \left(\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix}' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} \right) = \begin{bmatrix} 1 \\ 0 \\ 1 \\ 0 \end{bmatrix}.$$

Live growth:

$$\mathbf{l}_{P,2} = [(\mathbf{I}_L * (\mathbf{V}\mathbf{D})) + (\mathbf{I}_E * (\mathbf{V} - \mathbf{v}^E))]\widehat{\mathbf{S}}' \mathbf{1}$$

$$= \left\{ \left(\begin{bmatrix} 1 & 1 & 1 & 1 & 1 \\ 1 & 1 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 0 & 1 & 1 & 1 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} * \begin{bmatrix} 9 & 8 & 7 & 5 & 3 \\ 3 & 2 & 1 & 0 & 0 \\ 0 & 6 & 4 & 3 & 1 \\ 0 & 0 & 7 & 6 & 5 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} \right) \begin{bmatrix} 1 & 0 & 0 & 0 & 0 \\ -1 & 1 & 0 & 0 & 0 \\ 0 & -1 & 1 & 0 & 0 \\ 0 & 0 & -1 & 1 & 0 \\ 0 & 0 & 0 & -1 & 0 \end{bmatrix} \right\} \\ + \left\{ \left(\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} * \begin{bmatrix} 9 & 8 & 7 & 5 & 3 \\ 3 & 2 & 1 & 0 & 0 \\ 0 & 6 & 4 & 3 & 1 \\ 0 & 0 & 7 & 6 & 5 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} - \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} \right) \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{bmatrix}' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} \right\} \\ = \left\{ \left(\begin{bmatrix} 1 & 1 & 2 & 2 & 0 \\ 1 & 1 & 0 & 0 & 0 \\ 0 & 2 & 1 & 2 & 0 \\ 0 & 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} + \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \right) \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{bmatrix}' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} \right\} \\ = \left\{ \left(\begin{bmatrix} 1 & 1 & 2 & 2 & 0 \\ 1 & 1 & 0 & 0 & 0 \\ 0 & 2 & 1 & 2 & 0 \\ 0 & 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \right) \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{bmatrix}' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} \right\} = \left\{ \begin{bmatrix} 1 & 1 & 2 & 2 \\ 1 & 1 & 0 & 0 \\ 0 & 2 & 1 & 2 \\ 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 0 \end{bmatrix}' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} \right\} = \begin{bmatrix} 2 \\ 4 \\ 4 \\ 5 \end{bmatrix}.$$

Mortality:

$$\begin{aligned} \mathbf{m}_{p,2} &= [(\mathbf{I}_M * (\mathbf{V}\check{\mathbf{S}}))\check{\mathbf{S}}]'\mathbf{1} = \left\{ \left(\left[\begin{array}{ccccc} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{array} \right] * \left(\left[\begin{array}{ccccc} 9 & 8 & 7 & 5 & 3 \\ 3 & 2 & 1 & 0 & 0 \\ 0 & 6 & 4 & 3 & 1 \\ 0 & 0 & 7 & 6 & 5 \\ 1 & 0 & 0 & 0 & 0 \end{array} \right] \left[\begin{array}{ccccc} 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \end{array} \right] \right) \right) \left[\begin{array}{cccc} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{array} \right] \right\}' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} \\ &= \left[\left(\left[\begin{array}{ccccc} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{array} \right] * \left(\left[\begin{array}{ccccc} 8 & 7 & 5 & 3 & 0 \\ 2 & 1 & 0 & 0 & 0 \\ 6 & 4 & 3 & 1 & 0 \\ 0 & 7 & 6 & 5 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{array} \right] \right) \left[\begin{array}{cccc} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{array} \right] \right]' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} \\ &= \left\{ \left(\left[\begin{array}{ccccc} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 6 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{array} \right] \left[\begin{array}{cccc} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{array} \right] \right\}' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} = \left\{ \left[\begin{array}{ccccc} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 6 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{array} \right] \right\}' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} = \begin{bmatrix} 6 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}. \end{aligned}$$

Harvest:

$$\begin{aligned} \mathbf{h}_{p,2} &= [(\mathbf{I}_H \star (\mathbf{V}\check{\mathbf{S}}))\check{\mathbf{S}}]' \mathbf{1} = \left\{ \left(\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \star \begin{bmatrix} 9 & 8 & 7 & 5 & 3 \\ 3 & 2 & 1 & 0 & 0 \\ 0 & 6 & 4 & 3 & 1 \\ 0 & 0 & 7 & 6 & 5 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} \right) \begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \end{bmatrix} \right) \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{bmatrix} \right\}' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} \\ &= \left\{ \left(\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \star \begin{bmatrix} 8 & 7 & 5 & 3 & 0 \\ 2 & 1 & 0 & 0 & 0 \\ 6 & 4 & 3 & 1 & 0 \\ 0 & 7 & 6 & 5 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \right) \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{bmatrix} \right\}' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} \\ &= \left\{ \left(\begin{bmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 7 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \right) \begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{bmatrix} \right\}' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} = \left\{ \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 7 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \right\}' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} = \begin{bmatrix} 0 \\ 7 \\ 0 \\ 0 \\ 0 \end{bmatrix}. \end{aligned}$$

The total value vector at times P to 1:

$$\mathbf{v}_{P,1} = (\mathbf{I}_P * V)' \mathbf{1} = \left(\begin{bmatrix} 1 & 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 0 & 0 \\ 1 & 1 & 1 & 1 & 1 \\ 0 & 1 & 1 & 1 & 1 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} * \begin{bmatrix} 9 & 8 & 7 & 5 & 3 \\ 3 & 2 & 1 & 0 & 0 \\ 0 & 6 & 4 & 3 & 1 \\ 0 & 0 & 7 & 6 & 5 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} \right)' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} = \left(\begin{bmatrix} 9 & 8 & 7 & 5 & 3 \\ 3 & 2 & 1 & 0 & 0 \\ 0 & 6 & 4 & 3 & 1 \\ 0 & 0 & 7 & 6 & 5 \\ 1 & 0 & 0 & 0 & 0 \end{bmatrix} \right)' \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} = \begin{bmatrix} 13 \\ 16 \\ 19 \\ 14 \\ 9 \end{bmatrix}.$$

The estimands are compatible because:

$$\mathbf{v}_{P,2} - \mathbf{v}_{P-1,1} = \mathbf{e}_{P,2} + \mathbf{l}_{P,2} - \mathbf{m}_{P,2} - \mathbf{h}_{P,2} \Rightarrow \begin{bmatrix} 13 \\ 16 \\ 19 \\ 14 \end{bmatrix} - \begin{bmatrix} 16 \\ 19 \\ 14 \\ 9 \end{bmatrix} = \begin{bmatrix} 1 \\ 0 \\ 1 \\ 0 \end{bmatrix} + \begin{bmatrix} 2 \\ 4 \\ 4 \\ 5 \end{bmatrix} - \begin{bmatrix} 6 \\ 0 \\ 0 \\ 0 \end{bmatrix} - \begin{bmatrix} 0 \\ 7 \\ 0 \\ 0 \end{bmatrix} \Rightarrow \begin{bmatrix} -3 \\ -3 \\ 5 \\ 5 \end{bmatrix} = \begin{bmatrix} -3 \\ -3 \\ 5 \\ 5 \end{bmatrix}.$$